Please replace the paragraph beginning at page 55, line 1, with the following rewritten paragraph:

--**Construction of a hGH-substrate-phage vector**

The sequence of the linker region in pS0132 was mutated to create a substrate sequence for A64SAL subtilisin, using the oligonucleotide 5'-TTC-GGG-CCC-TTC-GCT-GCT-CAC-TAT-ACG-CGT-CAG-TCG-ACT-GAC-CTG-CCT-3' (SEQ ID NO:27). This resulted in the introduction of the protein sequence Phe-Gly-Pro-Phe-Ala-Ala-His-Tyr-Thr-Arg-Gln-Ser-Thr-Asp (SEQ ID NO:107) in the linker region between hGH and the carboxy terminal domain of gene III, where the first Phe residue in the above sequence is Phe191 of hGH. The sequence Ala-Ala-His-Tyr-Thr-Agr-Gln (SEQ ID NO:97) is known to be a good substrate for A64SAL subtilisin (Carter et al (1989), supra). The resulting plasmid was designated pS0640.--

B11

In the claims:

Please cancel claim 90 without prejudice or disclaimer.

Please amend claims 89, 91 and 92 as follows.

89. (Once Amended) A gene fusion, comprising a first gene encoding a first polypeptide, a second gene encoding at least a portion of a phage coat protein, and a suppressible termination codon between or adjacent to the first and second genes.

D12

91. (Once Amended) The gene fusion of claim 89, wherein the suppressible termination codon is UAG, UAA or UGA.

D13

92. (Once Amended) The gene fusion of claim 89, wherein the phage coat protein is a filamentous bacteriophage coat protein III or a portion thereof.